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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/496,444DATE: 03/01/2000  
TIME: 10:34:37

Input Set: I496444.RAW

<p>This Raw Listing contains the General Information Section and up to first 5 pages.</p>
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ENTERED

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1  <110> APPLICANT: Tao, Yumin
2      Gordon-Kamm William J.
3      Lowe, Keith S.
4      Bailey, Matthew A.
5  <120> TITLE OF INVENTION: Cell Cycle Polynucleotide, Polypeptide,
6      and Uses Thereof
7  <130> FILE REFERENCE: 1109
8  <140> CURRENT APPLICATION NUMBER: US/09/496,444
9  <141> CURRENT FILING DATE: 2000-02-02
10 <150> EARLIER APPLICATION NUMBER: US 60/119,857
11 <151> EARLIER FILING DATE: 1999-02-12
12 <150> EARLIER APPLICATION NUMBER: US 60/101,551
13 <151> EARLIER FILING DATE: 1998-09-23
14 <150> EARLIER APPLICATION NUMBER: US 09/398,858
15 <151> EARLIER FILING DATE: 1999-09-20
16 <150> EARLIER APPLICATION NUMBER: US 09/257,131
17 <151> EARLIER FILING DATE: 1999-02-25
18 <160> NUMBER OF SEQ ID NOS: 8
19 <170> SOFTWARE: FastSEQ for Windows Version 3.0
20 <210> SEQ ID NO 1
21 <211> LENGTH: 1636
22 <212> TYPE: DNA
23 <213> ORGANISM: Zea mays
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (109)...(1381)
27 <221> NAME/KEY: misc_feature
28 <222> LOCATION: (1)...(1636)
29 <223> OTHER INFORMATION: n = A,T,C or G
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32      gccgatccgt cttcttcccc tctcctgcg ggtcggcggt tggggatc atg gcg gcg      117
33                                     Met Ala Ala
34                                     1
35      cgg gcg gct gac gag aac agg aga ccg gcg gca ggg aag ccc gcg cca      165
36      Arg Ala Ala Asp Glu Asn Arg Arg Pro Ala Ala Gly Lys Pro Ala Pro
37      5              10              15
38      ggc gtc cga gac atg gcg agc cgg cgc gcg ctc acg gac atc aag aac      213
39      Gly Val Arg Asp Met Ala Ser Arg Arg Ala Leu Thr Asp Ile Lys Asn
40      20              25              30              35
41      ctc gtc ggg gct gcc ccg tac ccc tac gcc gtc gcc aag aag ccc atg      261
42      Leu Val Gly Ala Ala Pro Tyr Pro Tyr Ala Val Ala Lys Lys Pro Met
43      40              45              50
44      ctg cag aag agc aaa agg gac gaa aag cag cca gcg ttg gca agc agc      309

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45	Leu Gln Lys Ser Lys Arg Asp Glu Lys Gln Pro Ala Leu Ala Ser Ser	
46	55 60 65	
47	cgg ccc atg aca agg aaa ttc gcc gcc tcc ttg gcg agc aag ggc caa	357
48	Arg Pro Met Thr Arg Lys Phe Ala Ala Ser Leu Ala Ser Lys Gly Gln	
49	70 75 80	
50	cct gaa tgt cag ccg atc gta gct gat cca gaa ccc gaa gtt tgt caa	405
51	Pro Glu Cys Gln Pro Ile Val Ala Asp Pro Glu Pro Glu Val Cys Gln	
52	85 90 95	
53	cag aag gaa tca gta ggc gat ggc acc gtt gat att gac gtg gaa ctc	453
54	Gln Lys Glu Ser Val Gly Asp Gly Thr Val Asp Ile Asp Val Glu Leu	
55	100 105 110 115	
56	tac gag ctg gtc gac ggt agt gat agt gac atc gac atg ggt gcg aca	501
57	Tyr Glu Leu Val Asp Gly Ser Asp Ser Asp Ile Asp Met Gly Ala Thr	
58	120 125 130	
59	gag aac aag gac att atg aac gaa gat gaa ttg ctc atg gat att gac	549
60	Glu Asn Lys Asp Ile Met Asn Glu Asp Glu Leu Leu Met Asp Ile Asp	
61	135 140 145	
62	agt gca gac tcg ggg aac ccg ctt gct gca aca gaa tat gtt aaa gag	597
63	Ser Ala Asp Ser Gly Asn Pro Leu Ala Ala Thr Glu Tyr Val Lys Glu	
64	150 155 160	
65	ctt tac acc ttt tac aga gaa aat gag gct aag agt tgt gta agg cca	645
66	Leu Tyr Thr Phe Tyr Arg Glu Asn Glu Ala Lys Ser Cys Val Arg Pro	
67	165 170 175	
68	gat tac atg tcc agc caa caa gac ata aac tca aag atg aga gca att	693
69	Asp Tyr Met Ser Ser Gln Gln Asp Ile Asn Ser Lys Met Arg Ala Ile	
70	180 185 190 195	
71	ctg att gac tgg ctg att gag gtt cac tac aag ttt gaa ctg atg gat	741
72	Leu Ile Asp Trp Leu Ile Glu Val His Tyr Lys Phe Glu Leu Met Asp	
73	200 205 210	
74	gag acg ctc ttt ctt atg gta aac ata ata gat aga ttc ttg gaa aag	789
75	Glu Thr Leu Phe Leu Met Val Asn Ile Ile Asp Arg Phe Leu Glu Lys	
76	215 220 225	
77	gaa gtg gtt cca agg aag aag cta caa ctg gtt gga gtc aca gct atg	837
78	Glu Val Val Pro Arg Lys Lys Leu Gln Leu Val Gly Val Thr Ala Met	
79	230 235 240	
80	ctg ctc gct tgt aaa tat gag gag gta tct gtt cca gtt gtt gag gac	885
81	Leu Leu Ala Cys Lys Tyr Glu Glu Val Ser Val Pro Val Val Glu Asp	
82	245 250 255	
83	ctt gtg ctg ata tct gac cgt gcc tac aca aaa ggg caa att tta gaa	933
84	Leu Val Leu Ile Ser Asp Arg Ala Tyr Thr Lys Gly Gln Ile Leu Glu	
85	260 265 270 275	
86	atg gaa aag ttg att ctg aac acg ctg cag ttc aac atg tct gtt cca	981
87	Met Glu Lys Leu Ile Leu Asn Thr Leu Gln Phe Asn Met Ser Val Pro	
88	280 285 290	
89	aca cct tat gtc ttc atg aag agg ttt ctg aaa gct gca gat gca gat	1029
90	Thr Pro Tyr Val Phe Met Lys Arg Phe Leu Lys Ala Ala Asp Ala Asp	
91	295 300 305	
92	aaa cag ctt gag cta gcg tca ttt ttc atg ctg gag ctc tgc ttg gta	1077
93	Lys Gln Leu Glu Leu Ala Ser Phe Phe Met Leu Glu Leu Cys Leu Val	
94	310 315 320	

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# RAW SEQUENCE LISTING PATENT APPLICATION US/09/496,444

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95      gaa tac caa atg ctg aat tat cgg cct tcg cat ctg gct gct gct gcg      1125
96      Glu Tyr Gln Met Leu Asn Tyr Arg Pro Ser His Leu Ala Ala Ala Ala
97      325                      330                      335
98      gtt tat act gca cag tgt gct atc aat cgt tgc cag cac tgg aca aag      1173
99      Val Tyr Thr Ala Gln Cys Ala Ile Asn Arg Cys Gln His Trp Thr Lys
100     340                      345                      350                      355
101     gtc tgc gag tct cat agc aga tac act agc gac caa ctc ctg gag tgc      1221
102     Val Cys Glu Ser His Ser Arg Tyr Thr Ser Asp Gln Leu Leu Glu Cys
103                      360                      365                      370
104     tcg agg atg atg gta gat ttt cac cag aag gct gga acc agt aag ctc      1269
105     Ser Arg Met Met Val Asp Phe His Gln Lys Ala Gly Thr Ser Lys Leu
106                      375                      380                      385
107     act ggc gtg cac agg aag tac agt acc tac aag ttc ggt tgc gtg gcc      1317
108     Thr Gly Val His Arg Lys Tyr Ser Thr Tyr Lys Phe Gly Cys Val Ala
109                      390                      395                      400
110     aag att ttg cct gcg cag ttc ctg ctg gag tcg gga ggg aca ccg cct      1365
111     Lys Ile Leu Pro Ala Gln Phe Leu Leu Glu Ser Gly Gly Thr Pro Pro
112     405                      410                      415
113     cct tca ggt gca aac t agttgaatcg acctattcaa ctgggtggat tttttaagat      1421
114     Pro Ser Gly Ala Asn
115     420
116     ttttagaata ctccatgaac aagatgcaga aaacatcgtg ttgatgttgc ccaaaagtgc      1481
117     atcgaatttc tttggagagt tatgattaac aacttttttt ttatctatgt tgaatgacga      1541
118     gtgacggtcg gtcacgttgt gcttgtgcag ttatactgcg gctaataaca aactgtccag      1601
W--> 119     ttnttctnaa aaaaaaaaaa aaaaaaaaaa aaaaa      1636
120     <210> SEQ ID NO 2
121     <211> LENGTH: 424
122     <212> TYPE: PRT
123     <213> ORGANISM: Zea mays
124     <400> SEQUENCE: 2
125     Met Ala Ala Arg Ala Ala Asp Glu Asn Arg Arg Pro Ala Ala Gly Lys
126     1                      5                      10                      15
127     Pro Ala Pro Gly Val Arg Asp Met Ala Ser Arg Arg Ala Leu Thr Asp
128     20                      25                      30
129     Ile Lys Asn Leu Val Gly Ala Ala Pro Tyr Pro Tyr Ala Val Ala Lys
130     35                      40                      45
131     Lys Pro Met Leu Gln Lys Ser Lys Arg Asp Glu Lys Gln Pro Ala Leu
132     50                      55                      60
133     Ala Ser Ser Arg Pro Met Thr Arg Lys Phe Ala Ala Ser Leu Ala Ser
134     65                      70                      75                      80
135     Lys Gly Gln Pro Glu Cys Gln Pro Ile Val Ala Asp Pro Glu Pro Glu
136     85                      90                      95
137     Val Cys Gln Gln Lys Glu Ser Val Gly Asp Gly Thr Val Asp Ile Asp
138     100                     105                     110
139     Val Glu Leu Tyr Glu Leu Val Asp Gly Ser Asp Ser Asp Ile Asp Met
140     115                     120                     125
141     Gly Ala Thr Glu Asn Lys Asp Ile Met Asn Glu Asp Glu Leu Leu Met
142     130                     135                     140
143     Asp Ile Asp Ser Ala Asp Ser Gly Asn Pro Leu Ala Ala Thr Glu Tyr
144     145                     150                     155                     160

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145 Val Lys Glu Leu Tyr Thr Phe Tyr Arg Glu Asn Glu Ala Lys Ser Cys
146                               165                               170                               175
147 Val Arg Pro Asp Tyr Met Ser Ser Gln Gln Asp Ile Asn Ser Lys Met
148                               180                               185                               190
149 Arg Ala Ile Leu Ile Asp Trp Leu Ile Glu Val His Tyr Lys Phe Glu
150                               195                               200                               205
151 Leu Met Asp Glu Thr Leu Phe Leu Met Val Asn Ile Ile Asp Arg Phe
152                               210                               215                               220
153 Leu Glu Lys Glu Val Val Pro Arg Lys Lys Leu Gln Leu Val Gly Val
154                               225                               230                               235                               240
155 Thr Ala Met Leu Leu Ala Cys Lys Tyr Glu Glu Val Ser Val Pro Val
156                               245                               250                               255
157 Val Glu Asp Leu Val Leu Ile Ser Asp Arg Ala Tyr Thr Lys Gly Gln
158                               260                               265                               270
159 Ile Leu Glu Met Glu Lys Leu Ile Leu Asn Thr Leu Gln Phe Asn Met
160                               275                               280                               285
161 Ser Val Pro Thr Pro Tyr Val Phe Met Lys Arg Phe Leu Lys Ala Ala
162                               290                               295                               300
163 Asp Ala Asp Lys Gln Leu Glu Leu Ala Ser Phe Phe Met Leu Glu Leu
164                               305                               310                               315                               320
165 Cys Leu Val Glu Tyr Gln Met Leu Asn Tyr Arg Pro Ser His Leu Ala
166                               325                               330                               335
167 Ala Ala Ala Val Tyr Thr Ala Gln Cys Ala Ile Asn Arg Cys Gln His
168                               340                               345                               350
169 Trp Thr Lys Val Cys Glu Ser His Ser Arg Tyr Thr Ser Asp Gln Leu
170                               355                               360                               365
171 Leu Glu Cys Ser Arg Met Met Val Asp Phe His Gln Lys Ala Gly Thr
172                               370                               375                               380
173 Ser Lys Leu Thr Gly Val His Arg Lys Tyr Ser Thr Tyr Lys Phe Gly
174                               385                               390                               395                               400
175 Cys Val Ala Lys Ile Leu Pro Ala Gln Phe Leu Leu Glu Ser Gly Gly
176                               405                               410                               415
177 Thr Pro Pro Pro Ser Gly Ala Asn
178                               420

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179 <210> SEQ ID NO 3
180 <211> LENGTH: 21
181 <212> TYPE: DNA
182 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <221> NAME/KEY: primer_bind
185 <222> LOCATION: (1)...(21)
186 <400> SEQUENCE: 3
187 ctagtgttgca cctgaaggag g
188 <210> SEQ ID NO 4
189 <211> LENGTH: 22
190 <212> TYPE: DNA
191 <213> ORGANISM: Artificial Sequence
192 <220> FEATURE:
193 <221> NAME/KEY: primer_bind
194 <222> LOCATION: (1)...(22)

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RAW SEQUENCE LISTING  
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196      gctaagagtt gtgtaaggcc ag                22
197 <210> SEQ ID NO 5
198 <211> LENGTH: 21
199 <212> TYPE: DNA
200 <213> ORGANISM: Artificial Sequence
201 <220> FEATURE:
202 <221> NAME/KEY: primer_bind
203 <222> LOCATION: (1)...(21)
204 <400> SEQUENCE: 5
205      ttgggcaaca tcaacacgat g                21
206 <210> SEQ ID NO 6
207 <211> LENGTH: 23
208 <212> TYPE: DNA
209 <213> ORGANISM: Artificial Sequence
210 <220> FEATURE:
211 <221> NAME/KEY: primer_bind
212 <222> LOCATION: (1)...(23)
213 <400> SEQUENCE: 6
214      aaccgcgttg ctgcaacaga ata            23
215 <210> SEQ ID NO 7
216 <211> LENGTH: 23
217 <212> TYPE: DNA
218 <213> ORGANISM: articial organism
219 <220> FEATURE:
220 <221> NAME/KEY: primer_bind
221 <222> LOCATION: (1)...(23)
222 <400> SEQUENCE: 7
223      aatccaccca gttgaatagg tcg            23
224 <210> SEQ ID NO 8
225 <211> LENGTH: 23
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
228 <220> FEATURE:
229 <221> NAME/KEY: primer_bind
230 <222> LOCATION: (1)...(23)
231 <400> SEQUENCE: 8
232      atccgtcttc ttcccctcct cct            23
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VERIFICATION SUMMARY  
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DATE: 03/01/2000  
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Line ? Error/Warning

Original Text

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119 W "N" or "Xaa" used: Feature required

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ttntttctnaa aaaaaaaaaa aaaaaaaaaa aaaaaa